

H.S.

1652

2. Hulson 1004
 RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/269,860

DATE: 02/14/2001
 TIME: 16:03:08

Input Set : A:\4453us.ST25.txt
 Output Set: N:\CRF3\02142001\I269860.raw

3 <110> APPLICANT: Ankenbauer, Waltraud
 4 Schmitz-Aghegian, Gudrun
 5 Elizaveta, Bonch-Osmolovskaya
 6 Svetlichny, Vitaly
 7 Ebenbichler, Christine
 8 Angerer, Bernhard
 9 Laue, Frank
 11 <120> TITLE OF INVENTION: Thermostable Nucleic Acid Polymerase From Thermococcus gorgonarius
 13 <130> FILE REFERENCE: 4453
 15 <140> CURRENT APPLICATION NUMBER: US 09/269,860
 C--> 16 <141> CURRENT FILING DATE: 2000-03-10
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP97/05393
 19 <151> PRIOR FILING DATE: 1997-10-01
 21 <150> PRIOR APPLICATION NUMBER: EP/97100584.8
 22 <151> PRIOR FILING DATE: 1997-01-16
 24 <150> PRIOR APPLICATION NUMBER: EP/96115874.8
 25 <151> PRIOR FILING DATE: 1996-10-03
 27 <160> NUMBER OF SEQ ID NOS: 9
 29 <170> SOFTWARE: PatentIn version 3.0
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 33 <212> TYPE: DNA
 34 <213> ORGANISM: Artificial
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 37 <223> OTHER INFORMATION: probe
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_feature
 41 <222> LOCATION: (9)..(9)
 42 <223> OTHER INFORMATION: any nucleotide
 45 <220> FEATURE:
 46 <221> NAME/KEY: misc_feature
 47 <222> LOCATION: (15)..(15)
 48 <223> OTHER INFORMATION: any nucleotide
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 55 <210> SEQ ID NO: 2
 56 <211> LENGTH: 24
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 58 <213> ORGANISM: Artificial
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 64 ggcctacgag aggaacgaaac tggc
 67 <210> SEQ ID NO: 3
 68 <211> LENGTH: 18
 69 <212> TYPE: DNA
 70 <213> ORGANISM: Artificial

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82 <213> ORGANISM: Artificial
84 <220> FEATURE:
85 <223> OTHER INFORMATION: amplification primer
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93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial
96 <220> FEATURE:
97 <223> OTHER INFORMATION: amplification primer
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110 <222> LOCATION: (1)..(2322)
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115 1 5 10 15
117 agg atc ttc aag aag gag aac ggc gag ttc acc ata gac tac gac aga 96
118 Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Thr Ile Asp Tyr Asp Arg
119 20 25 30
121 aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct ccg att 144
122 Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Pro Ile
123 35 40 45
125 gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg 192
126 Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg
127 50 55 60
129 gtt gtc agg gcc gag aaa gtg aag aag ttc cta ggc agg ccg ata 240
130 Val Val Arg Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Pro Ile
131 65 70 75 80
133 gag gtc tgg aag ctc tac ttc act cac ccc cag gac gtt ccc gca atc 288
134 Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile
135 85 90 95
137 agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac 336
138 Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr
139 100 105 110

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142	Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	
143	115				120					125							
145	atg	gag	ggc	gac	gag	gaa	ctt	aag	atg	ctc	gcc	ttc	gac	atc	gag	acg	432
146	Met	Glu	Gly	Asp	Glu	Glu	Leu	Lys	Met	Leu	Ala	Phe	Asp	Ile	Glu	Thr	
147	130				135				140								
149	ctc	tat	cac	gag	ggc	gag	gag	ttc	gcc	gaa	ggg	cct	atc	ctg	atg	ata	480
150	Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Ala	Glu	Gly	Pro	Ile	Leu	Met	Ile	
151	145			150					155				160				
153	agc	tac	gcc	gac	gag	gaa	ggg	gcg	cgc	gtt	att	acc	tgg	aag	aat	atc	528
154	Ser	Tyr	Ala	Asp	Glu	Glu	Gly	Ala	Arg	Val	Ile	Thr	Trp	Lys	Asn	Ile	
155	165			170					175								
157	gac	ctt	ccc	tat	gtc	gac	gtc	gtt	tcc	acc	gag	aag	gag	atg	ata	aag	576
158	Asp	Leu	Pro	Tyr	Val	Asp	Val	Val	Ser	Thr	Glu	Lys	Glu	Met	Ile	Lys	
159	180			185					190								
161	cgc	ttc	ctc	aag	gtc	gtc	aag	gaa	aag	gat	ccc	gac	gtc	ctc	ata	atc	624
162	Arg	Phe	Leu	Lys	Val	Val	Lys	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Ile	
163	195			200					205								
165	tac	aac	ggc	gac	aac	ttc	gac	ttc	gcc	tac	ctc	aag	aag	cgc	tcc	gag	672
166	Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Phe	Ala	Tyr	Leu	Lys	Lys	Arg	Ser	Glu	
167	210			215					220								
169	aag	ctc	gga	gtc	aag	ttc	atc	ctc	gga	agg	gaa	ggg	agc	gaa	ccg	aaa	720
170	Lys	Leu	Gly	Val	Lys	Phe	Ile	Leu	Gly	Arg	Glu	Gly	Ser	Glu	Pro	Lys	
171	225			230					235				240				
173	atc	cag	cgc	atg	ggc	gat	cgc	ttt	gct	gtg	gag	gtc	aag	gga	agg	att	768
174	Ile	Gln	Arg	Met	Gly	Asp	Arg	Phe	Ala	Val	Glu	Val	Lys	Gly	Arg	Ile	
175	245			250					255								
177	cac	ttc	gac	ctc	tac	ccc	gtc	att	agg	aga	acg	att	aac	ctc	ccc	act	816
178	His	Phe	Asp	Leu	Tyr	Pro	Val	Ile	Arg	Arg	Thr	Ile	Asn	Leu	Pro	Thr	
179	260			265					270								
181	tac	acc	ctt	gag	gca	gtt	ata	gaa	gcc	atc	ttt	gga	cag	ccg	aag	gag	864
182	Tyr	Thr	Leu	Glu	Ala	Val	Tyr	Glu	Ala	Ile	Phe	Gly	Gln	Pro	Lys	Glu	
183	275			280					285								
185	aag	gtc	tac	gct	gag	gag	ata	gct	cag	gcc	tgg	gaa	acg	ggc	gag	gga	912
186	Lys	Val	Tyr	Ala	Glu	Glu	Ile	Ala	Gln	Ala	Trp	Glu	Thr	Gly	Glu	Gly	
187	290			295					300								
189	tta	gaa	agg	gtg	gcc	cgc	tac	tcg	atg	gag	gac	gct	aag	gta	acc	tat	960
190	Leu	Glu	Arg	Val	Ala	Arg	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Val	Thr	Tyr	
191	305			310					315				320				
193	gaa	ctc	gga	aaa	gag	ttc	tcc	cct	atg	gaa	gcc	cag	ctc	tcg	cgc	ctc	1008
194	Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu	
195	325			330					335								
197	gta	ggc	cag	agc	ctc	tgg	gat	gta	tct	cgc	tcg	agt	acc	gga	aac	ctc	1056
198	Val	Gly	Gln	Ser	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu	
199	340			345					350								
201	gtc	gag	tgg	ttt	ttg	ctg	agg	aag	gcc	tac	gag	agg	aat	gaa	ctt	gca	1104
202	Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala	
203	355			360					365								
205	cca	aac	aag	ccg	gac	gag	agg	ctg	gca	aga	aga	agg	gag	agc	tac		1152

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207	370					375			380								
209	gct	ggg	tac	gtc	aag	gag	ccc	gaa	agg	gga	ctg	tgg	gag	aac	atc	1200	
210	Ala	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Arg	Gly	Leu	Trp	Glu	Asn	Ile	
211	385					390			395			400					
213	gtg	tat	ctg	gac	ttc	cgc	tcc	ctg	tat	cct	tcg	ata	ata	atc	acc	cat	
214	Val	Tyr	Leu	Asp	Phe	Arg	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	His	
215						405			410			415					
217	aac	gtc	tcc	cct	gat	aca	ctc	aac	agg	gag	ggg	tgt	gaa	gag	tac	gac	
218	Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Glu	Glu	Tyr	Asp	
219						420			425			430					
221	gtg	gct	cct	cag	gtt	ggc	cat	aag	ttc	tgc	aag	gac	ttc	ccc	ggc	ttc	
222	Val	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe	
223						435			440			445					
225	atc	cca	agc	ctc	ctc	gga	gac	ctc	ttg	gag	gag	aga	cag	aag	gta	aag	
226	Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Val	Lys	
227						450			455			460					
229	aag	aag	atg	aag	gcc	act	ata	gac	cca	atc	gag	aag	aaa	ctc	ctc	gat	
230	Lys	Lys	Met	Lys	Ala	Thr	Ile	Asp	Pro	Ile	Glu	Lys	Lys	Leu	Leu	Asp	
231						465			470			475			480		
233	tac	agg	caa	cga	gca	atc	aaa	atc	ctt	gct	aat	agc	ttc	tac	ggt	tac	
234	Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	Tyr	
235						485			490			495					
237	tac	ggc	tat	aca	aag	gcc	cgc	tgg	tac	tac	aag	gag	tgc	gcc	gag	agc	
238	Tyr	Gly	Tyr	Thr	Lys	Ala	Arg	Trp	Tyr	Tyr	Lys	Glu	Cys	Ala	Glu	Ser	
239						500			505			510					
241	gtt	acc	ggg	tgg	ggc	agg	gag	tac	atc	gag	acc	acg	ata	agg	gaa	ata	
242	Val	Thr	Gly	Trp	Gly	Arg	Glu	Tyr	Ile	Glu	Thr	Thr	Ile	Arg	Glu	Ile	
243						515			520			525					
245	gag	gag	aaa	ttt	ggc	ttt	aaa	gtc	ctc	tac	gct	ggc	gac	aca	gat	gga	ttt
246	Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Phe	
247						530			535			540					
249	ttc	gca	aca	ata	cct	gga	gct	gac	gcc	gaa	acc	gtc	aaa	aag	aag	gca	
250	Phe	Ala	Thr	Ile	Pro	Gly	Ala	Asp	Ala	Glu	Thr	Val	Lys	Lys	Ala		
251						545			550			555			560		
253	aag	gag	tcc	ctg	gac	tac	atc	aac	gcc	aaa	ctg	ccc	ggc	ctg	ctc	gaa	
254	Lys	Glu	Phe	Leu	Asp	Tyr	Ile	Asn	Ala	Lys	Leu	Pro	Gly	Leu	Glu		
255						565			570			575					
257	ctc	gaa	tac	gag	ggc	ttc	tac	aag	cgc	ggc	ttc	ttc	gtg	acg	aag	aag	
258	Leu	Glu	Tyr	Gly	Phe	Tyr	Lys	Arg	Gly	Phe	Phe	Phe	Val	Thr	Lys	Lys	
259						580			585			590					
261	aag	tac	gct	ttt	ata	gac	gag	gag	gac	aag	ata	acg	acg	cgc	ggg	ctt	
262	Lys	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Asp	Lys	Ile	Thr	Thr	Arg	Gly	Leu	
263						595			600			605					
265	gaa	ata	gtt	agg	cgt	gac	tgg	agc	gag	ata	gct	aat	acg	acg	cgc	gct	
266	Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala	
267						610			615			620					
269	agg	gtt	ctt	gag	gct	ata	cta	aag	cac	ggt	gac	gtt	gaa	gaa	gct	gta	
270	Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala	Val	

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271	625	630	635	640	
273	agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca				1968
274	Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro				
275	645	650	655		
277	ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac				2016
278	Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp				
279	660	665	670		
281	tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca				2064
282	Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala				
283	675	680	685		
285	agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc				2112
286	Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu				
287	690	695	700		
289	aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt				2160
290	Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe				
291	705	710	715	720	
293	gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag				2208
294	Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln				
295	725	730	735		
297	gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa				2256
298	Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys				
299	740	745	750		
301	gaa gat tta agg tat cag aaa acg ccg cag gtt ggc ttg ggg gcg tgg				2304
302	Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp				
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305	cta aaa cct aag aca tga				2322
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307	770				
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311	<211> LENGTH: 773				
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313	<213> ORGANISM: Thermococcus gorgonarius				
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322	20	25	30		
325	Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Pro Ile				
326	35	40	45		
329	Glu Asp Val Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg				
330	50	55	60		
333	Val Val Arg Ala Glu Lys Val Lys Lys Phe Leu Gly Arg Pro Ile				
334	65	70	75	80	
337	Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Val Pro Ala Ile				
338	85	90	95		
341	Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr				
342	100	105	110		
345	Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro				
346	115	120	125		

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:52 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1